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Development and assessment of biotic stress tolerant cucumber hybrids using land races and commercial varieties

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ABSTRACT

Cucumber growers suffer significant economic losses due to yield reductions caused by pests such as fruit flies and diseases like powdery mildew and downy mildew. Therefore, one of the most effective ways to reduce losses caused by these pressures is to grow resistant cultivars. This study aimed to estimate important genetic parameters to approximate inbred line performance in the F1 generation and identify appropriate F1 cross combinations resistant to these biotic stresses. Thirty F1 hybrid combinations were screened, along with 13 parents (ten diverse stable lines and three testers) and a standard check. The genotypes UHF-CUC-11, UHF-CUC-13, UHF-CUC-6, UHF-CUC-15, UHF-CUC-8, Solan Srijan and F1 cross-combinations UHF-CUC-11 × Solan Srijan, UHF-CUC-13 × Solan Srijan, UHF-CUC-6 × K-75, UHF-CUC-15 × Solan Srijan and UHF-CUC-8 × Solan Srijan were found superior for these biotic stresses in the experimental results. Additionally, the predominance of non-additive gene activity due to genetic complementation between parents suggests that heterosis breeding could help enhance important biotic stress tolerance in cucumbers. The resistant genotypes and hybrid combinations identified in the current research can be employed to integrate the resistant genes into the preferred elite backgrounds of cucumber to develop biotic stress-resistant varieties/hybrids.

Key words: *Cucumis sativus* L.*,* Combining ability, Gene action, Heterosis, Resistance, Line × Tester.

INTRODUCTION

Cucumber is one of the important summer vegetables widely grown for the delicious soft fruits used commercially as salad ingredients, pickled condiments, sweets, and even brine (Jat *et al.*, 5). The cultivation period of this crop coincides with the onset of monsoon rains, favouring the development of various diseases that cause a substantial quality and economic yield loss throughout its growth and development. Fruit flies are the most dangerous pests since they may infest almost every cucurbit vegetable grown on every continent except Antarctica and the Arctic (Kapoor *et al.*, 6). However, B. cucurbitae is the most common of the fruit fly species known to attack cucurbits, and its presence is a major deterrent to the cultivation of cucumbers and other cucurbits, potentially to the point where such cultivation becomes economically unfeasible (Srinivas *et al.*, 16). Cucumber production is threatened in 80 nations around the world by pests like fruit flies, as well as by fungal diseases like powdery mildew and downy mildew, which can infect the leaves, stems, and fruits of open-field and greenhouse-grown cucumbers, respectively (Woltman *et al.*, 18). Conventionally, these biotic stresses in cucumbers have been mitigated through chemically based pesticides and fungicides. However, the excess use of chemicals to manage these biotic stresses and their presence in residual form makes them health hazardous as they are consumed mostly in fresh form. It may be most cost-effective and environmentally preferable to incorporate host plant resistance and grow resistant cultivars to reduce these biotic pressures. Despite widespread cultivation, economic significance, and common consumption of cucumbers as a popular vegetable in the country, the minimal focus has been on their genetic improvement for resistance against biotic stresses Kumari *et al.*, (9). Therefore, the present situation compels us to undertake this study. Hence, the success of any genetic improvement program depends on selecting genetically better parents and applying sound breeding techniques.

MATERIALS AND METHODS

The current study used 10 local lines with varying degrees of genetic diversity (Table 1) as well as three testers with a wide genetic base along with one standard check (Pusa Sanyog) in 2016, 30 F1 crosses were generated by crossing 10 lines and 3 testers in natural field conditions during the wet season. Seeds from the F1 population (30 plants) were sown in a randomized complete block design (RCBD) with three replications during the rainy season of the following year to evaluate the plants

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Table 1. Genotypes used and their sources of seed.

S. No.	Genotypes	Source	Sex form
1.	Line(s): UHF-CUC-4, UHF-CUC-6, UHF-CUC-7, UHF-CUC-8, UHF-CUC-9, UHF-CUC-11, UHF-CUC-12, UHF-CUC-13, UHF-CUC-14 UHF-CUC-15 K-75	Deptt. of Vegetable Science, UHF, Nauni, Solan, HP	Monoecious
2.	Tester(s): K-75, Poinsette and Solan Srijan	Deptt. of Vegetable Science, UHF, Nauni, Solan, HP	Monoecious
3.	Standard check cultivar: Pusa Sanyog	ICAR-IARI Regional Research Station, Katrain, Kullu, HP	Monoecious

for various biotic stress traits. The experimental plots had previously been deep ploughed and harrowed to obtain the fine tilth. A total of 16 plants were grown in a plot that measured 2.0 m × 4.0 m, with 100 × 50 cm of space between each row. The total number of fruits per plant and fruits infested with fruit flies were counted from the 10 randomly selected plants from each entry to work out the incidence of fruit flies as per the following formula:

$$\text{Incidence of fruit fly (\%)} = \frac{\text{Number of fruit fly infested fruits}}{\text{Total number of fruits}} \times 100$$

The occurrence and severity of powdery and downy mildew (%) were recorded periodically under natural field conditions by randomly selecting fifteen leaves from different height levels (from top to bottom) from 10 vines of each replication of every parent and cross combination. Powdery mildew severity was recorded using the 0-5 scale proposed by Ransom *et al.* (14), and downy mildew severity was noted using the 0-4 scale suggested by Reuveni (15). The disease severity index (%) in both diseases was calculated using McKinney's formula (12).

$$\text{Disease severity index (\%)} = \frac{\Sigma(n \times v)}{Z \times N} \times 100$$

Where,
n= number of leaves in each category
v= numerical value of each category
Z= numerical value of highest category
N=Total number of leaves in sample

According to the experimental design, the data were analyzed with MS-Excel, OPSTAT, and the SPAR 2.0 software, and analysis of variance was used to estimate mean performance, combining ability (general and specific), gene action, and proportional contribution.

RESULTS AND DISCUSSION

One of the vegetable breeder's primary goals is to develop new varieties/hybrids that are superior to the existing ones concerning biotic stresses. For example, there was a large difference in fruit fly incidence (parents=8.68-19.27 and hybrids=4.33-18.57%), powdery mildew severity (parents=7.13-16.17 and hybrids=4.46-16.64%), and severity of downy mildew (parents=8.26-20.38 and hybrids=5.16-17.61%) between the parents and the hybrids (Table 2). Twenty-five out of thirty (F1) hybrids had fruit fly, powdery, and downy mildew infestation rates lower than the control Pusa Sanyog. Thus, the genotypes viz., UHF-CUC-11, UHF-CUC-13, UHF-CUC-6, UHF-CUC-15, UHF-CUC-8 and Solan Srijan and hybrids UHF-CUC-11 × Solan Srijan, UHF-CUC-13 × Solan Srijan, UHF-CUC-6 × K-75, UHF-CUC-15 × Solan Srijan, UHFCUC-8 × Solan Srijan and UHF-CUC-7 × Poinsette from existing collections can serve as resistant sources in future breeding projects because to their extensive variability for various biotic stressors. Also, farmers can use these hybrid combinations directly after their multilocational yield trials. The outcome of the present study is consistent with the findings of Call *et al.* (3), Kumar *et al.* (7), and Kumari *et al.* (8).

Selecting parents based on per se performance alone is inadequate to guarantee the birth of offspring with a high frequency of transgressive genes despite being the conventional method Allard (1). To determine whether or not there are significant differences in combining ability among genotypes (lines, tests, and crosses), a general analysis of variance was performed, and the results are summarized in Table 3. Estimating combining ability helps breeders pick inbred lines and detect heterotic crossings early in the breeding process, which is important for estimating the worth of cucumber lines for imposing improvement. "When it comes to assessing the impacts of lines and testers on general combining ability (GCA), as well as the effects of cross combinations on specialized combining ability (sca), Line × Tester analysis stands out as one of the most effective biometrical methods available. Successful prediction of the genetic potentiality of crosses, which yield desirable individuals in a segregating population of cross-pollinated crops, is aided by the gca analysis, which provides estimates of the average performance of a line in hybrid combination and indicates the genetic differences that exist among the lines being

Table 2. Mean performance of top five parents and hybrids (F_1) for different biotic stress traits.

Traits	Range		Mean ± SE	Top five parents	Top five cross combinations (F_1)
	Parents	Hybrids			
IFF	8.68 to 19.27	4.33 to 18.57	11.06 ± 0.31	Solan Srijan (8.68) K-75(9.55) UHF-CUC-13(11.48) UHF-CUC-11(11.61) UHF-CUC-6 (12.00)	UHF-CUC-11×Solan Srijan (4.33) UHF-CUC-13×Solan Srijan (4.37) UHF-CUC-6×K-75 (4.84) UHF-CUC-15×Solan Srijan (4.90) UHF-CUC-8×K-75 (5.21)
SPM	7.13 to 16.17	4.46 to 16.64	9.82 ± 0.59	UHF-CUC-11 (7.13) UHF-CUC-13 (7.31) K-75 (8.50) Solan Srijan (8.52) UHF-CUC-15 (8.75)	UHF-CUC-15×Solan Srijan (4.46) UHF-CUC-13×Solan Srijan (4.52) UHF-CUC-11×Solan Srijan (4.57) UHF-CUC-6×K-75 (4.58) UHF-CUC-6×Poinsette (5.14)
SDM	8.26 to 20.38	5.16 to 17.61	10.97 ± 0.48	Solan Srijan (8.26) K-75 (8.49) UHF-CUC-13(10.54) UHF-CUC-11(10.92) UHF-CUC-6 (11.14)	UHF-CUC-11×Solan Srijan (5.16) UHF-CUC-15×Solan Srijan (5.25) UHF-CUC-13×Solan Srijan (5.28) UHF-CUC-6×K-75 (5.52) UHF-CUC-8×Solan Srijan (5.56)

Whereas, IFF = Incidence of fruit fly, SPM = Severity of powdery mildew and SDM = Severity of downy mildew

Table 3. Estimates of general combining ability (GCA) and specific combining ability (SCA) effects.

Traits	Top significant desirable parents	Top significant desirable cross combinations
Incidence of fruit fly	UHF-CUC-11 (-2.55) UHF-CUC-15 (-2.14) UHF-CUC-13 (-2.05) UHF-CUC-6 (-1.88) Solan Srijan (-1.71)	UHF-CUC-12×Solan Srijan (-5.20) UHF-CUC-14×Poinsette (-3.69) UHF-CUC-7×K-75 (-2.51) UHF-CUC-13×Poinsette (-2.38) UHF-CUC-9×K-75 (-2.36)
Severity of powdery mildew	UHF-CUC-6 (-3.65) UHF-CUC-15 (-2.31) UHF-CUC-13 (-1.70) UHF-CUC-11 (-1.38) Solan Srijan (-0.72)	UHF-CUC-12×K-75 (-4.60) UHF-CUC-9×K-75 (-4.38) UHF-CUC-14×Poinsette (-4.34) UHF-CUC-8×Solan Srijan (-3.41) UHF-CUC-11× Solan Srijan (-2.71)
Severity of downy mildew	UHF-CUC-11 (-2.76) UHF-CUC-8 (-2.10) UHF-CUC-15 (-1.82) UHF-CUC-12 (-1.41) UHF-CUC-6 (-1.30)	UHF-CUC-9×Poinsette (-5.40) UHF-CUC-7×K-75 (-2.64) UHF-CUC-13×Solan Srijan (-2.50) UHF-CUC-12×Poinsette (-1.86) UHF-CUC-15×Solan Srijan (-1.75)

evaluated. Due to their strong negative GCA effects, the 13 genotypes UHF-CUC-11, UHF-CUC-15, UHF-CUC-13, UHF-CUC-6, Solan Srijan, and K-75 were identified as promising candidates for use as general combiners in reducing the prevalence of fruit fly and the intensity of powdery and downy mildews, respectively (Table 3). It appears that parents with a good or high GCA effect are more likely to have genes that contribute to the relevant traits, making this a valid criterion for predicting SCA. The selected lines from these numerous crossings could be distributed as conventional varieties or employed as better parents in F1 hybrid production programmes to generate more disease-resistant or phenotypically diverse offspring. If one parent has a high GCA and the other does not, then the hybrid offspring from that cross will have the highest sca estimate for the characteristic of interest (Cruz *et al.*, 4). Hybrids that are less sensitive to plant diseases are sought after. Therefore, in this case, the parents should be those with complementary genes that, when recombined in the development of the hybrid, confer reduced illness values, as shown by negative gca and sca values. There were 30 possible cross-combinations, but only 14 were deemed good specific cross-combinations because of their strong negative SCA impacts on fruit fly incidence and powdery and downy severity, respectively (Table 3). In terms of fruit fly incidence, the top five cross combinations involved parents with poor×good, average×poor, poor×good, good×poor, and poor× good gca effects, as follows: UHF-CUC-12×Solan Srijan (-5.20), UHF-CUC-14×Poinsette (-3.69), UHF-CUC-7×K-75 (-2.51), UHF-CUC-13×Poinsette (-2.38) and UHF-CUC-9×K-75 (-2.36). UHF-CUC-12×K-75 (-4.60), UHF-CUC-9×K-75 (-4.38), UHF-CUC-14×Poinsette (-4.34), UHF-CUC-8×Solan Srijan (-3.41), and UHF-CUC-11×Solan Srijan (-2.71) were the best cross combinations for powdery mildew resistance involved parents with poor × good, poor × good, average × poor, poor × good and good × good GCA effects, respectively. Primary crosses involving parents with poor×poor, poor×good, good×good, good×poor, and good×good GCA effects were UHF-CUC-9×Poinsette (-5.40), UHF-CUC-7×K-75 (-2.64), UHF-CUC-13×Solan Srijan (-2.50), UHF-CUC-12×Poinsette (-1.86), and UHF-CUC-15×Solan Srijan (-1.75) for severity of downy mildew. The importance of the SCA effect clarifies genetic diversity among the tested parents. It shows how dominance and epistasis contribute to the genetic variation connected to heterosis, both of which are fixed. High sca effect crosses did not always have parents with high GCA effects, highlighting the significance of intra- and inter-allelic interactions. Lack of complementation between parent genes may explain why hybrids with high GCA effects on some traits but low sca effects on others were created by parents with strong GCA effects. Contrarily, hybrids with large SCA effects can be traced back to the complementary gene impact in parents with low GCA effects. In early generations (F2), transgressive segregants can be obtained from crossings where both parents have good good×gca effects. When creating superior variants via the pedigree method, hybrid combinations with good average gca effects in the parents should be evaluated since they may produce desirable transgressive segregants in later segregating generations. The best crosses for heterosis breeding to improve cucumber genetics are those with good and bad GCA effects since these show the presence of both additive and non-additive genetic variations. However, hybrid vigour can also be exploited commercially through crosses with high sca effects involving a poor combiner and a poor parent, as the non-additive, non-fixable genes appear to play a larger role in these crosses. Earlier researchers, like Brar *et al.* (2), Kumar *et al.* (7), and Kumari *et al.* (8), revealed significant negative gca and sca impacts of diverse parental material for these biotic stressors in cucumbers.

Adopting a suitable breeding methodology for the purposeful management of generated variability, mainly dependent upon the type of gene action in the population for the traits under genetic improvement, is the next crucial step in a dynamic breeding programme after identifying appropriate parents and potential crosses. The extent to which genes are expressed depends on each parent's genetic makeup and history. Differences in variance estimates for GCA and SCA shed light on the character of gene action. Indicating the predominance of non-additive gene action governed in these traits, the estimates of s2 SCA were larger than s2 GCA (average), and the dominance (s2s) components of variance were significant compared to the additive (s2g) components, indicating the great potential for heterosis breeding in cucumber. Table 4 shows that the variance ratio is less than 1 for all parameters, including fruit fly incidence (0.75), powdery mildew severity (0.02), and downy mildew prevalence (0.74). Non-additive gene action was found to be affecting nearly all of the features in the cucumber. With an understanding of the GCA and SCA variances, as well as the additive (s2A) and dominant (s2D) components of variance, one might conclude that non-additive gene effects predominate in cucumber and that the vegetable can be improved through hybridization/hybrid breeding.

Table 5 presents the relative contributions of lines, testers, and their interactions to F1. For both fruit fly incidence (36.07%) and downy mildew severity (42.88%), the contribution of lines was higher than the individual contribution of testers and lines×tester's interactions. For these biotic stress variables, it showed that the lines differed more in their GCA variance estimates, indicating additive gene activity. The lower estimates of particular

Table 4. Estimates of genetic components of variance for different biotic stress traits.

Traits	σ^2 GCA (Lines)	σ^2 GCA (Testers)	σ^2 GCA (Average)	σ^2 SCA	σ^2g	σ^2s	σ^2g/σ^2s (Variance ratio)
IFF	3.65	7.03	6.25	8.29	25.0	33.16	0.75
SPM	0.90	-0.04	0.17	10.64	0.70	42.55	0.02
SDM	3.84	4.47	4.32	5.87	17.28	23.49	0.74

Whereas, IFF = Incidence of fruit fly (%), SPM = Severity of powdery mildew (%) and SDM = Severity of downy mildew (%)

Table 5. Proportional contribution of lines, testers and their interactions to sum of squares of crosses.

Character(s)	Per cent contribution of		
	Lines	Testers	Lines × Testers
Incidence of fruit fly (%)	36.07	32.61	31.31
Severity of powdery mildew (%)	35.98	6.18	57.83
Severity of downy mildew (%)	42.88	27.48	29.64

combining ability variance can be explained by the contribution of lines×tester's interactions being lower than lines or testers for traits. However, the contribution of lines×testers was determined to be greater than that of lines and testers interactions individually (57.83%) regarding the severity of powdery mildew. The present results are at odds with those of Kumar *et al.* (5), who found that the contribution of lines was greatest for the severity of powdery mildew, while the contribution of testers was greatest for the incidence of fruit flies and the severity of downy mildew.

The concentration of beneficial dominant alleles in the F1 population causes heterosis, the superiority of F1 above the mean of the parents or over the better parent or the standard check. Estimates of heterosis for all traits showed statistically significant variation among cross combinations (Table 6). Out of 30 hybrid combinations, significant desirable negative heterosis for incidence of fruit fly, the severity of powdery and downy mildew was recorded in 17 & 23; 9 & 9 and 16 & 11 F1 crosses over better parent and standard check cultivar, respectively. Negative heterosis for fruit fly incidence, powdery and downy mildew severity in cucumber was also documented by Brar *et al.* (2), Kumar *et al.* (7), Kumari *et al.* (8), Sharma (11) and Thakur *et al.* (17). As a result, hybrid vigour could be used commercially to enhance these qualities in cucumber. The substantial heterosis response seen in most hybrids provided strong evidence for a non-additive component in the inheritance of the feature under study. Cultivating resistant or tolerant varieties is a good strategy to reduce losses from diseases and insect attacks. These lines can be effectively used when resistance is needed against specific biotic stresses. Heterosis breeding enables the combination of desired alleles in a more immediate and predictable manner compared to the longer-term process required for developing open-pollinated cultivars Kumari *et al.*, (10).

AUTHORS' CONTRIBUTION

Conceptualization of research and designing of the experiment (Ramesh K), execution of field/ lab

Table 6. Estimates of heterosis (F_1) over better parent and standard check.

Traits	Incidence of fruit fly	Severity of powdery mildew	Severity of downy mildew
Range of heterosis over better parent (%)	-54.66 to 74.35	-47.65 to 95.31	-37.53 to 113.20
No. of significant desirable crosses over better parent	17	9	16
Per cent increase or decrease over better parent (%)	UHF-CUC-11×Solan Srijan (-54.66) UHF-CUC-13×Solan Srijan (-54.24) UHF-CUC-15×Solan Srijan (-48.69) UHF-CUC-12×Solan Srijan (-45.45) UHF-CUC-6 × K-75(-44.24)	UHF-CUC-15×Solan Srijan (-47.65) UHF-CUC-6×K-75(-46.12) UHF-CUC-14×Poinsette(-44.14) UHF-CUC-6×Poinsette(-43.95) UHF-CUC-11×Solan Srijan (-35.90)	UHF-CUC-11×Solan Srijan (-37.53) UHF-CUC-15×Solan Srijan (-36.44) UHF-CUC-13×Solan Srijan (-36.08) UHF-CUC-12×Poinsette(-35.88) UHF-CUC-6×Poinsette(-34.98)
Range of heterosis over standard check (%)	-65.80 to 46.68	-47.03 to 97.62	-46.97 to 80.99
No. of significant desirable crosses over standard check	23	9	12
Per cent increase or decrease over standard check (%)	UHF-CUC-11×Solan Srijan (-65.80) UHF-CUC-13×Solan Srijan (-65.48) UHF-CUC-15×Solan Srijan (-61.30) UHF-CUC-8×K-75 (-58.85) UHF-CUC-6×K-75 (-44.24)	UHF-CUC-15×Solan Srijan (-47.03) UHF-CUC-13×Solan Srijan (-46.32) UHF-CUC-11×Solan Srijan (-45.72) UHF-CUC-6×K-75(-45.61) UHF-CUC-6×Poinsette(-38.95)	UHF-CUC-11×Solan Srijan (-46.97) UHF-CUC-15×Solan Srijan (-46.04) UHF-CUC-13×Solan Srijan (-45.73) UHF-CUC-6×Poinsette(-43.27) UHF-CUC-8×Solan Srijan (-42.86)

experiments and data collection, analysis of data and interpretation (Reena K), contribution in preparation of the manuscript (Rajeev K, AC and KS).

DECLARATION

The authors do not have any conflict of interest.

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